

#8



1

EXPRESS MAIL NO. EL755728058US

## SEQUENCE LISTING

<110> White, Aaron P.  
Doran, James L.  
Collinson, S. Karen  
Kay, William W.

<120> BACTERIAL FIMBRIAL SYSTEM FOR  
PRESENTATION OF HETEROLOGOUS PEPTIDE SEQUENCES

<130> 920043.406

<140> US 09/543,407  
<141> 2000-04-05

<160> 59

<170> FastSEQ for Windows Version 4.0

<210> 1  
<211> 456  
<212> DNA  
<213> Salmonella enteritidis

<400> 1

atgaaaacttt	taaaagtggc	agcattcgca	gcaatcgtag	tttctggcag	tgctctggct	60
ggcgtcgttc	cacaatgggg	ccggcgccgt	aatcataacg	cgccgcggcaa	tagttccggc	120
cccgactcaa	cgtttagcat	ttatcgtac	ggttccgcta	acgctgcgt	tgctctgcaa	180
agcgatgcc	gtaaatctga	aacgaccatt	acccagagcg	gttatggtaa	cgccgcccgt	240
gtaggccagg	gtgcggataa	tagtactatt	gaactgactc	agaatggttt	cagaataaat	300
gccaccatcg	accaggggaa	cgctaaaaac	tccgatatta	ctgtcggcca	atacggcggt	360
aataacgccc	cgctggtaa	tcagaccgca	tctgattcca	gcgtaatgg	gcgtcagggt	420
ggttttggca	acaacgcccac	ggctaaccag	tattaa			456

<210> 2  
<211> 456  
<212> DNA  
<213> Salmonella enteritidis

<400> 2

atgaaaaaca	aattgttatt	tatgtatgg	acaatactgg	gtgcgcctgg	gattgcaacc	60
gccccacaatt	atgatctggc	tcgttcagaa	tataattttg	cggtaaatga	attaagcaag	120
tcttcattta	atcaggcggc	cattattgt	caagtccgca	cggtataatag	tgccagagta	180
cggccaggaag	gatcaaaact	attgtccgtt	atttcacaag	aaggaggaaa	taatcgggccc	240
aaaatcgacc	aggcaggaa	ttataacttt	gcgtatattg	agcaaacggg	caatgccaac	300
gatgccagta	tatcgaaaag	cgcttacggt	aataagtgcag	ctattatcca	gaaaggttct	360
ggaaataagg	ccaatattac	ccagtacggt	acgcagaaaa	cagcagttgt	agtgcagaaa	420
cagtcgcata	tggctattcg	cgtcacccaa	cgctaa			456

<210> 3

<211> 456  
<212> DNA  
<213> E. Coli

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<400> 3
atgaaacttt taaaagtaga agcaattgca gcaatcgat tctccggtag cgctctggca 60
ggtgtgttc ctcagtgacgg cgccggcggt aaccacggtg gtggcggtaa taatagcggc 120
ccaaattctg agctgaacat ttaccagtac ggtggcggtta actctgcact tgctctgcaa 180
actgatgccc gtaactctga cttgacttatt acccagcatg gcggcggtaa tggtgcat 240
gttggtcagg gctcagatga cagctcaatc gatctgaccc aacgtggctt cggttaacacg 300
gctactcttg atcagtggaa cggcaaaaat tctgaaatga cggttaaacaca gttcggtgg 360
ggcaacggtg ctgcagttga ccagactgca tctaactcct ccgtcaacgt gactcagggtt 420
ggctttggta acaacgcgac cgctcatcag tactaa 456

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<210> 4  
<211> 456  
<212> DNA  
<213> E. Coli

<400> 4  
atgaaaaaaca aattgttatt tatgatgtta acaatactgg gtgcgcctgg gattgcagcc 60  
gcagcagggtt atgatttagc taattcagaa tataacttcg cggttaaatga attgagtaag 120  
tcttcattta atcaggcagc cataattggt caagctggg ctaataatag tgctcagtt 180  
cggcaggggag gctcaaaaact tttggcgggtt gttgcgcagaag aaggttagtag caaccgggca 240  
aagattgacc agacaggaga ttataacctt gcatatatggt atcaggcggg cagtgcac 300  
gatgccagta ttgcgaagg tgcttatggt aataactgcga tgattatcca gaaaggttct 360  
ggtaataaaag caaatattac acagtatggt actaaaaaaaaa cggttttgtt agtgcagaga 420  
cagtcgcaaa tggttattcg cgtgacacaa cgttaa 456

<210> 5  
<211> 151  
<212> PRT  
<213> *Salmonella enteritidis*

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<400> 5
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
      1           5                   10          15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Asn His
      20          25                   30
Asn Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35          40                   45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
      50          55                   60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
      65          70                   75          80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85          90                   95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100         105                  110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115         120                  125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130         135                  140
Asn Ala Thr Ala Asn Gln Tyr

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145 150

<210> 6  
<211> 151  
<212> PRT  
<213> Salmonella enteritidis

<400> 6

Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro  
1 5 10 15  
Gly Ile Ala Thr Ala Thr Asn Tyr Asp Leu Ala Arg Ser Glu Tyr Asn  
20 25 30  
Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile  
35 40 45  
Ile Gly Gln Val Gly Thr Asp Asn Ser Ala Arg Val Arg Gln Glu Gly  
50 55 60  
Ser Lys Leu Leu Ser Val Ile Ser Gln Glu Gly Gly Asn Asn Arg Ala  
65 70 75 80  
Lys Val Asp Gln Ala Gly Asn Tyr Asn Phe Ala Tyr Ile Glu Gln Thr  
85 90 95  
Gly Asn Ala Asn Asp Ala Ser Ile Ser Gln Ser Ala Tyr Gly Asn Ser  
100 105 110  
Ala Ala Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln  
115 120 125  
Tyr Gly Thr Gln Lys Thr Ala Val Val Val Gln Lys Gln Ser His Met  
130 135 140  
Ala Ile Arg Val Thr Gln Arg  
145 150

<210> 7  
<211> 151  
<212> PRT  
<213> Escherichia coli

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<400> 7
Met Lys Leu Leu Lys Val Ala Ala Ile Ala Ala Ile Val Phe Ser Gly
      1           5           10          15
Ser Ala Leu Ala Gly Val Val Pro Gln Tyr Gly Gly Gly Asn His
      20          25          30
Gly Gly Gly Asn Asn Ser Gly Pro Asn Ser Glu Leu Asn Ile Tyr
      35          40          45
Gln Tyr Gly Gly Asn Ser Ala Leu Ala Leu Gln Thr Asp Ala Arg
      50          55          60
Asn Ser Asp Leu Thr Ile Thr Gln His Gly Gly Asn Gly Ala Asp
      65          70          75          80
Val Gly Gln Gly Ser Asp Asp Ser Ser Ile Asp Leu Thr Gln Arg Gly
      85          90          95
Phe Gly Asn Ser Ala Thr Leu Asp Gln Trp Asn Gly Lys Asn Ser Glu
      100         105         110
Met Thr Val Lys Gln Phe Gly Gly Asn Gly Ala Ala Val Asp Gln
      115         120         125
Thr Ala Ser Asn Ser Ser Val Asn Val Thr Gln Val Gly Phe Gly Asn
      130         135         140
Asn Ala Thr Ala His Gln Tyr

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145                    150

<210> 8  
<211> 151  
<212> PRT  
<213> Escherichia coli

<400> 8  
Met Lys Asn Lys Leu Leu Phe Met Met Leu Thr Ile Leu Gly Ala Pro  
1                        5                        10                        15  
Gly Ile Ala Ala Ala Gly Tyr Asp Leu Ala Asn Ser Glu Tyr Asn  
20                        25                        30  
Phe Ala Val Asn Glu Leu Ser Lys Ser Ser Phe Asn Gln Ala Ala Ile  
35                        40                        45  
Ile Gly Gln Ala Gly Thr Asn Asn Ser Ala Gln Leu Arg Gln Gly Gly  
50                        55                        60  
Ser Lys Leu Leu Ala Val Val Ala Gln Glu Gly Ser Ser Asn Arg Ala  
65                        70                        75                        80  
Lys Ile Asp Gln Thr Gly Asp Tyr Asn Leu Ala Tyr Ile Asp Gln Ala  
85                        90                        95  
Gly Ser Ala Asn Asp Ala Ser Ile Ser Gln Gly Ala Tyr Gly Asn Thr  
100                      105                        110  
Ala Met Ile Ile Gln Lys Gly Ser Gly Asn Lys Ala Asn Ile Thr Gln  
115                      120                        125  
Tyr Gly Thr Gln Lys Thr Ala Ile Val Val Gln Arg Gln Ser Gln Met  
130                      135                        140  
Ala Ile Arg Val Thr Gln Arg  
145                      150

<210> 9  
<211> 48  
<212> DNA  
<213> Leishmania major

<400> 9  
tatgatcagc tggttacccg tgggttacc catgaaatgg cacatgca

48

<210> 10  
<211> 16  
<212> PRT  
<213> Leishmania major

<400> 10  
Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala  
1                        5                        10                        15

<210> 11  
<211> 456  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Recombinant Salmonella enteritidis 3b afgA  
sequence containing the replacement fragment

encoding PT3 from GP63 of Leishmania major.

<400> 11						
atgaaaacttt	taaaagtggc	agcattcgca	gcaatcgtag	tttctggcag	tgctctggct	60
ggcgtcggttc	cacaatgggg	cggcggcggt	aatcataacg	gcggcggcaa	tagttccggc	120
ccggactcaa	cgttgagcat	ttatcagtac	ggttccgcta	acgctgcgt	tgctctgcaa	180
agcgatgccc	gtaaatctga	aacgaccatt	acccagagcg	gttatggtaa	cggcgccgat	240
gtaggccagg	gtgcggataa	tagtactatt	gaactgactc	agaatggtt	cagaataat	300
gccaccatcg	accagtggaa	cgctaaaaac	tccgatatta	ctgtcggcca	atacggcggt	360
aataacgccc	cgctggttaa	ttatgatcag	ctggttaccc	gtgttgtac	ccatgaaatg	420
gcacatgcaa	acaacgccac	ggctaaccag	tattaa			456

<210> 12

<211> 151

<212> PRT

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from *Leishmania major*.

<400> 12

Met	Lys	Leu	Leu	Lys	Val	Ala	Ala	Phe	Ala	Ala	Ile	Val	Val	Ser	Gly
1														15	
Ser	Ala	Leu	Ala	Gly	Val	Val	Pro	Gln	Trp	Gly	Gly	Gly	Asn	His	
															20
Asn	Gly	Gly	Asn	Ser	Ser	Gly	Pro	Asp	Ser	Thr	Leu	Ser	Ile	Tyr	
															35
Gln	Tyr	Gly	Ser	Ala	Asn	Ala	Ala	Leu	Ala	Leu	Gln	Ser	Asp	Ala	Arg
															50
Lys	Ser	Glu	Thr	Thr	Ile	Thr	Gln	Ser	Gly	Tyr	Gly	Asn	Gly	Ala	Asp
															65
Val	Gly	Gln	Gly	Ala	Asp	Asn	Ser	Thr	Ile	Glu	Leu	Thr	Gln	Asn	Gly
															85
Phe	Arg	Asn	Asn	Ala	Thr	Ile	Asp	Gln	Trp	Asn	Ala	Lys	Asn	Ser	Asp
															100
Ile	Thr	Val	Gly	Gln	Tyr	Gly	Gly	Asn	Asn	Ala	Ala	Leu	Val	Asn	Tyr
															115
Asp	Gln	Leu	Val	Thr	Arg	Val	Val	Thr	His	Glu	Met	Ala	His	Ala	Asn
															130
Asn	Ala	Thr	Ala	Asn	Gln	Tyr									
															145
															150

<210> 13

<211> 456

<212> DNA

<213> Artificial Sequence

<220>

<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from *Leishmania major*.

<400> 13  
atgaaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct 60  
ggcgtcggtt cacaatgggg cggccggcgg aatcataacg gcggccgcaa tagttccggc 120  
ccggactcaa cggtgagcat ttatcagtgac gggtccgcta acgctgcgct tgctctgcaa 180  
agcgatgccc gtaaatctga aacgaccatt acccagagcg gttatggtaa cggccggat 240  
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggtt cagaataat 300  
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atatgatcg 360  
ctggttaccc gtgttggta ccatgaaatg gcacatgcaa gcgtaatggt gcgtcagggt 420  
ggtttggca acaacgcccc ggctaaaccag tattaa 456

<210> 14  
<211> 151  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 14  
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly  
1 5 10 15  
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Asn His  
20 25 30  
Asn Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr  
35 40 45  
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg  
50 55 60  
Lys Ser Glu Thr Thr Ile Gln Ser Gly Tyr Gly Asn Gly Ala Asp  
65 70 75 80  
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly  
85 90 95  
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp  
100 105 110  
Ile Thr Val Gly Gln Tyr Asp Gln Leu Val Thr Arg Val Val Thr His  
115 120 125  
Glu Met Ala His Ala Ser Val Met Val Arg Gln Val Gly Phe Gly Asn  
130 135 140  
Asn Ala Thr Ala Asn Gln Tyr  
145 150

<210> 15  
<211> 456  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 15  
atgaaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct 60

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ggcgtctatg atcagctgg taccctgttt gttacccatg aaatggcaca tgcacccggc 120  
ccggactcaa cgttggcat ttatcgtac gggtccgcta acgctgcgt tgctctgaa 180  
agcgatccc gtaaatctga aacgaccatt acccgagcg gttatggtaa cggcgccat 240  
gttaggccagg gtgcggataa tagtactatt gaactgactc agaatggttt cagaataat 300  
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt 360  
aataacgccc cgctggtaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggt 420  
ggtttggca acaacgcccc ggcttaaccag tattaa 456
```

<210> 16  
<211> 151  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

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<400> 16
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
      1           5           10          15
Ser Ala Leu Ala Gly Val Tyr Asp Gln Leu Val Thr Arg Val Val Thr
      20          25          30
His Glu Met Ala His Ala Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35          40          45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
      50          55          60
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp
65           70          75          80
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85          90          95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100         105         110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115         120         125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130         135         140
Asn Ala Thr Ala Asn Gln Tyr
      145         150

```

<210> 17  
<211> 456  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

```

<400> 17
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct      60
ggcgtcgttc cacaatgggg cgccggcggt aatcataacg gcggcggcaa tagttccggc      120
ccqgactatq atcaqctqgt taccctgtt qttacccatq aaatggcaca tqcactqcaa      180

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agcgatgcc	gtaaaatctga	aacgaccatt	acccagagcg	gttatggtaa	cggcgccgat	240
gttaggcagg	gtgcggataa	tagtactatt	gaactgactc	agaatggttt	cagaataaat	300
gccaccatcg	accagtggaa	cgctaaaaac	tccgatatta	ctgtcgccca	atacggcggt	360
aataacgccc	cgctggtaa	tcagaccgca	tctgattcca	gcgtaatgg	gcgtcaggtt	420
ggtttggca	acaacccac	ggctaaccag	tattaa			456

<210> 18  
<211> 151  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

<400> 18						
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly						
1	5	10	15			
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Asn His						
20	25	30				
Asn Gly Gly Asn Ser Ser Gly Pro Asp Tyr Asp Gln Leu Val Thr						
35	40	45				
Arg Val Val Thr His Glu Met Ala His Ala Leu Gln Ser Asp Ala Arg						
50	55	60				
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp						
65	70	75	80			
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly						
85	90	95				
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp						
100	105	110				
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln						
115	120	125				
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn						
130	135	140				
Asn Ala Thr Ala Asn Gln Tyr						
145	150					

<210> 19  
<211> 456  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

<400> 19						
atgaaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct						60
ggcgtcgttc cacaatgggg cggcgccggt aatcataacg gcggcgccaa tagtccggc						120
ccggactcaa cgttgagcat ttatcgtac gggtccgcta acgctgcgt tgctctgcaa						180
agcgatgcc gtaaatatga tcagctggtt acccggtttt ttacccatga aatggcacat						240
gcaggccagg gtgcggataa tagtactatt gaactgactc agaatggtt cagaataaat						300

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gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt 360
aataacgcgg cgtggtaa tcagaccgca tctgattcca gcgtaatggt gcgtcaggtt 420
ggttttggca acaacgcccc ggctaaaccag tattaa 456

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<210> 20  
<211> 151  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

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<400> 20
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly
      1           5           10          15
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Asn His
      20          25          30
Asn Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr
      35          40          45
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg
      50          55          60
Lys Tyr Asp Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His
      65          70          75          80
Ala Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly
      85          90          95
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Ser Asp
      100         105         110
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln
      115         120         125
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn
      130         135         140
Asn Ala Thr Ala Asn Gln Tyr
      145         150

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<210> 21
<211> 456
<212> DNA
<213> Artificial Sequence
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<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

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<400> 21
atgaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct 60
ggcgtcgttc cacaatgggg cgccggcggt aatcataacg gcggcgccaa tagttccggc 120
ccggactcaa cgttggcat ttatcgtac ggttccgcta acgctgcgt tgctctgcaa 180
agcgatgccc gttaaatctga aacgaccatt acccagagcg gttatggtaa cggcgccgat 240
gttaggccagg gtgcggataa ttatgatcg ctggttaccc gtgttggtaa ccatgaaatag 300
gcacatgcag accagtggaa cgctaaaaac tccgatattt ctgtcggcca atacggcggt 360
aataacqccq cgctqgtaa tcagaccqca tctgattcca gcgtaatggg gcgtcagggt 420
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ggtttggca acaacgcccc ggcttaaccag tattaa	456
<210> 22	
<211> 151	
<212> PRT	
<213> Artificial Sequence	
 <220>	
<223> Recombinant <i>Salmonella enteritidis</i> 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of <i>Leishmania major</i> .	
 <400> 22	
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly	
1 5 10 15	
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Asn His	
20 25 30	
Asn Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr	
35 40 45	
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg	
50 55 60	
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp	
65 70 75 80	
Val Gly Gln Gly Ala Asp Asn Tyr Asp Gln Leu Val Thr Arg Val Val	
85 90 95	
Thr His Glu Met Ala His Ala Asp Gln Trp Asn Ala Lys Asn Ser Asp	
100 105 110	
Ile Thr Val Gly Gln Tyr Gly Gly Asn Asn Ala Ala Leu Val Asn Gln	
115 120 125	
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn	
130 135 140	
Asn Ala Thr Ala Asn Gln Tyr	
145 150	
 <210> 23	
<211> 456	
<212> DNA	
<213> Artificial Sequence	
 <220>	
<223> Recombinant <i>Salmonella enteritidis</i> 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of <i>Leishmania major</i> .	
 <400> 23	
atgaaaacttt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct	60
ggcgctcggtt cacaatgggg cggcgccgtt aatcataacg gcggcgccaa tagttccggc	120
ccggactcaa cggtgagcat ttatcagttac gggtccgcta acgctgcgt tgctctgcaa	180
agcgatgccc gttaaatctga aacgaccatt acccagagcg gttatggtaa cggcgccgtt	240
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggtt cagaataaat	300
gccaccatcg accagtggaa cgctaaaaac tatgtatcgc tggttacccg tggttacc	360
catgaaatgg cacatgcaaa tcagaccgca tctgattcca gcgtaatggt gcgtcagggtt	420
ggtttggca acaacgcccc ggcttaaccag tattaa	456

<210> 24  
<211> 151  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

<400> 24  
Met Lys Leu Leu Lys Val Ala Ala Phe Ala Ala Ile Val Val Ser Gly  
1 5 10 15  
Ser Ala Leu Ala Gly Val Val Pro Gln Trp Gly Gly Gly Asn His  
20 25 30  
Asn Gly Gly Asn Ser Ser Gly Pro Asp Ser Thr Leu Ser Ile Tyr  
35 40 45  
Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln Ser Asp Ala Arg  
50 55 60  
Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly Asn Gly Ala Asp  
65 70 75 80  
Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu Thr Gln Asn Gly  
85 90 95  
Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp Asn Ala Lys Asn Tyr Asp  
100 105 110  
Gln Leu Val Thr Arg Val Val Thr His Glu Met Ala His Ala Asn Gln  
115 120 125  
Thr Ala Ser Asp Ser Ser Val Met Val Arg Gln Val Gly Phe Gly Asn  
130 135 140  
Asn Ala Thr Ala Asn Gln Tyr  
145 150

<210> 25  
<211> 456  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

<400> 25  
atgaaaactt taaaagtggc agcattcgca gcaatcgtag tttctggcag tgctctggct 60  
ggcgctcggt cacaatgggg cggcggcggt aatcataacg gcggcggcaa tagttccggc 120  
ccggactcaa cgttgagcat ttatcagtc acgctgcgt ttatgtatcag 180  
ctggttacc cgttgttac ccatgaaatg gcacatgcag gttatggtaa cggcgccgat 240  
gtaggccagg gtgcggataa tagtactatt gaactgactc agaatggtt cagaataat 300  
gccaccatcg accagtggaa cgctaaaaac tccgatatta ctgtcggcca atacggcggt 360  
aataacgccc cgctggttaa tcagaccgca tctgattcca gcgtaatggt gcgtcaggtt 420  
ggttttggca acaacgccac ggctaaccag tattaa 456

<210> 26  
<211> 151

<212> PRT  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 26

Met	Lys	Leu	Leu	Lys	Val	Ala	Ala	Phe	Ala	Ala	Ile	Val	Val	Val	Ser	Gly
1				5					10						15	
Ser	Ala	Leu	Ala	Gly	Val	Val	Pro	Gln	Trp	Gly	Gly	Gly	Gly	Asn	His	
				20				25						30		
Asn	Gly	Gly	Asn	Ser	Ser	Gly	Pro	Asp	Ser	Thr	Leu	Ser	Ile	Tyr		
	35				40					45						
Gln	Tyr	Gly	Ser	Ala	Asn	Ala	Ala	Leu	Tyr	Asp	Gln	Leu	Val	Thr	Arg	
	50				55					60						
Val	Val	Thr	His	Glu	Met	Ala	His	Ala	Gly	Tyr	Gly	Asn	Gly	Ala	Asp	
65				70					75					80		
Val	Gly	Gln	Gly	Ala	Asp	Asn	Ser	Thr	Ile	Glu	Leu	Thr	Gln	Asn	Gly	
	85					90					95					
Phe	Arg	Asn	Asn	Ala	Thr	Ile	Asp	Gln	Trp	Asn	Ala	Lys	Asn	Ser	Asp	
	100					105					110					
Ile	Thr	Val	Gly	Gln	Tyr	Gly	Gly	Asn	Asn	Ala	Ala	Leu	Val	Asn	Gln	
	115					120					125					
Thr	Ala	Ser	Asp	Ser	Ser	Val	Met	Val	Arg	Gln	Val	Gly	Phe	Gly	Asn	
	130					135					140					
Asn	Ala	Thr	Ala	Asn	Gln	Tyr										
	145				150											

<210> 27  
<211> 456  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Recombinant *Salmonella enteritidis* 3b afgA  
sequence containing the replacement fragment  
encoding PT3 from GP63 of *Leishmania major*.

<400> 27

atgaaaactt	taaaagtggc	agcattcgca	gcaatcgtag	tttctggcag	tgctctggct	60
ggcgctgttc	cacaatgggg	ccgcggcggt	aatcataacg	gcggcgccaa	tagttccggc	120
ccggactcaa	cgttgagcat	ttatcagtagc	gttcccgcta	acgctgcgct	tgctctgcaa	180
agcgatgcc	gtaaatctga	aacgaccatt	acccagagcg	gttatggtaa	cggcgccgat	240
tatgatcagc	tggttacccg	tgttgttacc	catgaaatgg	cacatgcatt	cagaataaat	300
gccaccatcg	accagtggaa	cgctaaaaac	tccgatatta	ctgtcgccca	atacggcggt	360
aataacgccc	cgctggttaa	tcaagaccgca	tctgattcca	gcgtaatgg	gcgtcagggt	420
ggttttggca	acaacgcccac	ggctaaccag	tattaa			456

<210> 28  
<211> 151  
<212> PRT  
<213> Artificial Sequence

&lt;220&gt;

<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

&lt;400&gt; 28

Met	Lys	Leu	Leu	Lys	Val	Ala	Ala	Phe	Ala	Ala	Ile	Val	Val	Ser	Gly
1				5					10					15	
Ser	Ala	Leu	Ala	Gly	Val	Val	Pro	Gln	Trp	Gly	Gly	Gly	Asn	His	
				20				25					30		
Asn	Gly	Gly	Gly	Asn	Ser	Ser	Gly	Pro	Asp	Ser	Thr	Leu	Ser	Ile	Tyr
				35			40				45				
Gln	Tyr	Gly	Ser	Ala	Asn	Ala	Leu	Ala	Leu	Gln	Ser	Asp	Ala	Arg	
				50			55				60				
Lys	Ser	Glu	Thr	Thr	Ile	Thr	Gln	Ser	Gly	Tyr	Gly	Asn	Gly	Ala	Asp
				65			70			75			80		
Tyr	Asp	Gln	Leu	Val	Thr	Arg	Val	Val	Thr	His	Glu	Met	Ala	His	Ala
				85			90			95					
Phe	Arg	Asn	Asn	Ala	Thr	Ile	Asp	Gln	Trp	Asn	Ala	Lys	Asn	Ser	Asp
				100			105				110				
Ile	Thr	Val	Gly	Gln	Tyr	Gly	Gly	Asn	Asn	Ala	Ala	Leu	Val	Asn	Gln
				115			120				125				
Thr	Ala	Ser	Asp	Ser	Ser	Val	Met	Val	Arg	Gln	Val	Gly	Phe	Gly	Asn
				130			135			140					
Asn	Ala	Thr	Ala	Asn	Gln	Tyr									
				145			150								

&lt;210&gt; 29

&lt;211&gt; 456

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Recombinant *Salmonella enteritidis* 3b afgA sequence containing the replacement fragment encoding PT3 from GP63 of *Leishmania major*.

&lt;400&gt; 29

atgaaaacttt	taaaagtggc	agcattcgca	gcaatcgtag	tttctggcag	tgctctggct	60
ggcgtcgttc	cacaatgggg	cgccggcggt	aatcataacg	gcggcgccaa	tagtccggc	120
ccggactcaa	cgttgagcat	ttatcagtagc	gttcccgcta	acgctgcgct	tgctctgcaa	180
agcgatgcc	gtaaatctga	aacgaccatt	acccagagcg	gttatggtaa	cggcgccgat	240
gtaggccagg	gtgcggataa	tagtactatt	gaactgactc	agaatggttt	cagaataataat	300
gcccacat	atcagctgg	tacccgtgtt	gttacccatg	aaatggcaca	tgcaggcggt	360
aataacgccc	cgctggttaa	tcagaccgca	tctgattcca	gcgtaatgg	gcgtcaggtt	420
ggttttggca	acaacgcccac	ggctaaccag	tattaa			456

&lt;210&gt; 30

&lt;211&gt; 151

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Recombinant *Salmonella enteritidis* 3b afgA  
 sequence containing the replacement fragment  
 encoding PT3 from GP63 of *Leishmania major*.

<400> 30

Met	Lys	Leu	Leu	Lys	Val	Ala	Ala	Phe	Ala	Ala	Ile	Val	Val	Ser	Gly
1				5					10					15	
Ser	Ala	Leu	Ala	Gly	Val	Val	Pro	Gln	Trp	Gly	Gly	Gly	Gly	Asn	His
					20				25					30	
Asn	Gly	Gly	Gly	Asn	Ser	Ser	Gly	Pro	Asp	Ser	Thr	Leu	Ser	Ile	Tyr
					35			40				45			
Gln	Tyr	Gly	Ser	Ala	Asn	Ala	Ala	Leu	Ala	Leu	Gln	Ser	Asp	Ala	Arg
					50			55			60				
Lys	Ser	Glu	Thr	Thr	Ile	Thr	Gln	Ser	Gly	Tyr	Gly	Asn	Gly	Ala	Asp
					65			70		75				80	
Val	Gly	Gln	Gly	Ala	Asp	Asn	Ser	Thr	Ile	Glu	Leu	Thr	Gln	Asn	Gly
					85				90				95		
Phe	Arg	Asn	Asn	Ala	Thr	Tyr	Asp	Gln	Leu	Val	Thr	Arg	Val	Val	Thr
					100				105			110			
His	Glu	Met	Ala	His	Ala	Gly	Gly	Asn	Asn	Ala	Ala	Leu	Val	Asn	Gln
					115				120			125			
Thr	Ala	Ser	Asp	Ser	Ser	Val	Met	Val	Arg	Gln	Val	Gly	Phe	Gly	Asn
					130			135			140				
Asn	Ala	Thr	Ala	Asn	Gln	Tyr									
					145			150							

<210> 31

<211> 131

<212> PRT

<213> *Salmonella enteritidis*

<400> 31

Gly	Val	Val	Pro	Gln	Trp	Gly	Gly	Gly	Asn	His	Asn	Gly	Gly	Gly
1				5				10				15		
Asn	Ser	Ser	Gly	Pro	Asp	Ser	Thr	Leu	Ser	Ile	Tyr	Gln	Tyr	Gly
					20			25			30			
Ala	Asn	Ala	Ala	Leu	Ala	Leu	Gln	Ser	Asp	Ala	Arg	Lys	Ser	Glu
					35			40			45			
Thr	Ile	Thr	Gln	Ser	Gly	Tyr	Gly	Asn	Gly	Ala	Asp	Val	Gly	Gln
					50			55			60			
Ala	Asp	Asn	Ser	Thr	Ile	Glu	Leu	Thr	Gln	Asn	Gly	Phe	Arg	Asn
					65			70		75			80	
Ala	Thr	Ile	Asp	Gln	Trp	Asn	Ala	Lys	Asn	Ser	Asp	Ile	Thr	Val
					85			90			95			
Gln	Tyr	Gly	Gly	Asn	Asn	Ala	Ala	Leu	Val	Asn	Gln	Thr	Ala	Ser
					100			105			110			
Ser	Ser	Val	Met	Val	Arg	Gln	Val	Gly	Phe	Gly	Asn	Asn	Ala	Thr
					115			120			125			
Asn	Gln	Tyr			130									

<210> 32

<211> 70

<212> PRT

<213> *Salmonella enteritidis*

<400> 32

Ala	Arg	Lys	Ser	Glu	Thr	Thr	Ile	Thr	Gln	Ser	Gly	Tyr	Gly	Asn	Gly
1				5				10					15		
Ala	Asp	Val	Gly	Gln	Gly	Ala	Asp	Asn	Ser	Thr	Ile	Glu	Leu	Thr	Gln
				20				25					30		
Asn	Gly	Phe	Arg	Asn	Asn	Ala	Thr	Ile	Asp	Gln	Trp	Asn	Lys	Asn	Asp
				35				40				45			
Ile	Val	Gly	Tyr	Gly	Asn	Ala	Leu	Asn	Thr	Ser	Asp	Ser	Val	Met	Val
				50				55				60			
Arg	Val	Gly	Ala	Asn	Tyr										
	65			70											

<210> 33

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus sequence of the five internal repeats of AgfA.

<221> VARIANT

<222> (1)...(23)

<223> Xaa = Any Amino Acid

<400> 33

Ser	Xaa	Xaa	Xaa	Xaa	Xaa	Gln	Xaa	Gly	Xaa	Xaa	Asn	Xaa	Ala	Xaa	Xaa
1						5			10				15		
Xaa	Gln	Xaa	Xaa	Ala	Xaa	Xaa									
				20											

<210> 34

<211> 109

<212> PRT

<213> *Salmonella enteritidis*

<400> 34

Ser	Thr	Leu	Ser	Ile	Tyr	Gln	Tyr	Gly	Ser	Ala	Asn	Ala	Ala	Leu	Ala
1				5				10					15		
Leu	Gln	Ser	Asp	Ala	Arg	Lys	Ser	Glu	Thr	Thr	Ile	Thr	Gln	Ser	Gly
				20				25					30		
Tyr	Gly	Asn	Gly	Ala	Asp	Val	Gly	Gln	Gly	Ala	Asp	Asn	Ser	Thr	Ile
				35				40				45			
Glu	Leu	Thr	Gln	Asn	Gly	Phe	Arg	Asn	Asn	Ala	Thr	Ile	Asp	Gln	Trp
				50				55				60			
Asn	Ala	Lys	Asn	Ser	Asp	Ile	Thr	Val	Gly	Gln	Tyr	Gly	Gly	Asn	Asn
				65				70			75			80	
Ala	Ala	Leu	Val	Asn	Gln	Thr	Ala	Ser	Asp	Ser	Ser	Val	Met	Val	Arg
				85				90					95		
Gln	Val	Gly	Phe	Gly	Asn	Asn	Ala	Thr	Ala	Asn	Gln	Tyr			
				100				105							

<210> 35  
<211> 109  
<212> PRT  
<213> Escherichia coli

<400> 35  
Ser Glu Leu Asn Ile Tyr Gln Tyr Gly Gly Gly Asn Ser Ala Leu Ala  
1 5 10 15  
Leu Gln Thr Asp Ala Arg Asn Ser Asp Leu Thr Ile Thr Gln His Gly  
20 25 30  
Gly Gly Asn Gly Ala Asp Val Gly Gln Gly Ser Asp Asp Ser Ser Ile  
35 40 45  
Asp Leu Thr Gln Arg Gly Phe Gly Asn Ser Ala Thr Leu Asp Gln Trp  
50 55 60  
Asn Gly Lys Asn Ser Glu Met Thr Val Lys Gln Phe Gly Gly Asn  
65 70 75 80  
Gly Ala Ala Val Asp Gln Thr Ala Ser Asn Ser Ser Val Asn Val Thr  
85 90 95  
Gln Val Gly Phe Gly Asn Asn Ala Thr Ala His Gln Tyr  
100 105

<210> 36  
<211> 56  
<212> PRT  
<213> Serratia marcescens

<400> 36  
Ile Glu Asn Ala Ile Gly Gly Ser Gly Asn Asp Val Ile Val Gly Asn  
1 5 10 15  
Ala Ala Asn Asn Val Leu Lys Gly Gly Ala Gly Asn Asp Val Leu Phe  
20 25 30  
Gly Gly Gly Ala Asp Glu Leu Trp Gly Gly Ala Gly Lys Asp Ile  
35 40 45  
Phe Val Phe Ser Ala Ala Ser Asp  
50 55

<210> 37  
<211> 68  
<212> PRT  
<213> Salmonella enteritidis

<400> 37  
Ser Thr Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala  
1 5 10 15  
Leu Gln Ser Asp Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly  
20 25 30  
Tyr Gly Asn Gly Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile  
35 40 45  
Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln Trp  
50 55 60  
Asn Ala Lys Asn  
65

<210> 38

<211> 47  
<212> PRT  
<213> bovine

<400> 38  
Val Ile Ile Ser Lys Lys Gly Asp Ile Ile Thr Ile Arg Thr Glu Ser  
1 5 10 15  
Pro Phe Lys Asn Thr Glu Ile Ser Phe Lys Leu Gly Gln Glu Phe Glu  
20 25 30  
Glu Thr Thr Ala Asp Asn Arg Lys Thr Lys Ser Thr Val Thr Leu  
35 40 45

<210> 39  
<211> 48  
<212> PRT  
<213> Salmonella enteritidis

<400> 39  
Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln  
1 5 10 15  
Ser Asp Ala Arg Lys Ser Glu Thr Thr Ile Thr Gln Ser Gly Tyr Gly  
20 25 30  
Asn Gly Ala Asp Val Gly Gln Gly Ala Asp Asn Ser Thr Ile Glu Leu  
35 40 45

<210> 40  
<211> 19  
<212> PRT  
<213> Unknown

<220>  
<223> Beta-prism motif of the vitelline membrane outer  
layer protein I (VMO-I)

<400> 40  
Phe Ala Leu Lys Val Glu Pro Ser Gln Phe Gly Arg Asp Asp Thr Ala  
1 5 10 15  
Leu Asn Gly

<210> 41  
<211> 19  
<212> PRT  
<213> Unknown

<220>  
<223> Beta-prism motif of the vitelline membrane outer  
layer protein I (VMO-I)

<400> 41  
Phe Ser Leu Arg Ser Glu Lys Ser Gln Gly Gly Gly Asp Asp Thr Ala  
1 5 10 15  
Ala Asn Asn

<210> 42  
<211> 19  
<212> PRT  
<213> Unknown

<220>  
<223> Beta-prism motif of the vitelline membrane outer  
layer protein I (VMO-I)

<400> 42  
Leu Gln Thr Lys Val Glu Ser Pro Gln Gly Leu Arg Asp Asp Thr Ala  
1 5 10 15  
Leu Asn Asn

<210> 43  
<211> 16  
<212> PRT  
<213> Unknown

<220>  
<223> Beta-prism motif of the vitelline membrane outer  
layer protein I (VMO-I)

<400> 43  
Leu Ser Ile Tyr Gln Tyr Gly Ser Ala Asn Ala Ala Leu Ala Leu Gln  
1 5 10 15

<210> 44  
<211> 16  
<212> PRT  
<213> Unknown

<220>  
<223> Beta-prism motif of the vitelline membrane outer  
layer protein I (VMO-I)

<400> 44  
Ile Glu Leu Thr Gln Asn Gly Phe Arg Asn Asn Ala Thr Ile Asp Gln  
1 5 10 15

<210> 45  
<211> 16  
<212> PRT  
<213> Unknown

<220>  
<223> Beta-prism motif of the vitelline membrane outer  
layer protein I (VMO-I)

<400> 45  
Val Met Val Arg Gln Val Gly Phe Gly Asn Asn Ala Thr Ala Asn Gln  
1 5 10 15

<210> 46  
<211> 143  
<212> PRT  
<213> *Salmonella enteritidis*

<400> 46

Ala	Gly	Phe	Val	Gly	Asn	Lys	Ala	Val	Val	Gln	Ala	Ala	Val	Thr	Ile
1									10					15	
Ala	Ala	Gln	Asn	Thr	Thr	Ser	Ala	Asn	Trp	Ser	Gln	Asp	Pro	Gly	Phe
									25					30	
Thr	Gly	Pro	Ala	Val	Ala	Ala	Gly	Gln	Lys	Val	Gly	Thr	Leu	Ser	Ile
									35					45	
Thr	Ala	Thr	Gly	Pro	His	Asn	Ser	Val	Ser	Ile	Ala	Gly	Lys	Gly	Ala
									40					60	
Ser	Val	Ser	Gly	Gly	Val	Ala	Thr	Val	Pro	Phe	Val	Asp	Gly	Gln	Gly
									65					80	
Gln	Pro	Val	Phe	Arg	Gly	Arg	Ile	Gln	Gly	Ala	Asn	Ile	Asn	Asp	Gln
									85					95	
Ala	Asn	Thr	Gly	Ile	Asp	Gly	Leu	Ala	Gly	Trp	Arg	Val	Ala	Ser	Ser
									100					110	
Gln	Glu	Thr	Leu	Asn	Val	Pro	Val	Thr	Thr	Phe	Gly	Lys	Ser	Thr	Leu
									115					125	
Pro	Ala	Gly	Phe	Thr	Ala	Thr	Phe	Tyr	Val	Gln	Gln	Tyr	Gln	Asn	
									130					140	

<210> 47  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 47

ttgaaattct	tcttaaattt	ttaaaatggc	gttgagtat	39
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<210> 48  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 48

acatgagcc	atttcatgtg	taacaacacg	tgtaacgagc	tgatcatatg	caatagtaac	60
cgctgcctga	accactgc					78

<210> 49  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 49  
tatgatcagc tcgttacacg tggtttaca catgaaatgg ctcatgctgg gcctgctgtt  
gctgctggtc agaaaaggtt 60  
78

<210> 50  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 50  
attaagctta tacataatcc ctctttaagt ttttgcatg 39

<210> 51  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 51  
gcagaattca gcagttgttag tgcagaaaaca gtcgcata 39

<210> 52  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 52  
tgcatgtgcc atttcatggg taacaacacg ggtaaccagc tgatcatagt ttttagcg  
ccactggtcg atgggtggc 60  
78

<210> 53  
<211> 78  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> PCR primer

<400> 53  
tatgatcagc tggttacccg tggtttacc catgaaatgg cacatgcaaa tcagaccgca  
tctgattcca gcttaatg 60  
78

<210> 54

<211> 39	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> PCR primer	
<400> 54	
agacgcaagc ttcgtttaat gtgacctgag ggatcacccg	39
<210> 55	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> PCR primer	
<400> 55	
gggatgttgt gtaaaagataa aaaaatagtg	30
<210> 56	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> PCR primer	
<400> 56	
tgcctaattct taggccataa tatttttgtg	30
<210> 57	
<211> 33	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> PCR primer	
<400> 57	
aggaaaggatc aaaactattt tccgttattt cac	33
<210> 58	
<211> 33	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> PCR primer	
<400> 58	
tatatttaca ctaagacgag acaactcaat cg	33

<210> 59  
<211> 18  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Consensus sequence

<221> VARIANT  
<222> (1)...(18)  
<223> Xaa = Any Amino Acid

<400> 59  
Ser Xaa Xaa Xaa Xaa Xaa Gln Xaa Gly Xaa Xaa Asn Xaa Ala Xaa Xaa  
1 5 10 15  
Xaa Gln